

Supporting Information

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SI Text

Cell Culture and Transfection. All cells were maintained in DMEM supplemented with 10% FBS in a humidified atmosphere of 5% CO₂ at 37 °C. All of the reagents and media used in cell culture were purchased from Invitrogen. The siRNA targeting TP53 (p53 siRNA) and its corresponding control (control siRNA) were purchased from Dharmacon. Transient transfection of expression plasmids or siRNA was mediated by Lipofectamine 2000 reagents (Invitrogen) according to the manufacturer's instructions.

RT-PCR. Total RNA was extracted from experimental cells by using RNeasy Mini Kit (Qiagen). First-strand cDNA was then synthesized by using the Omniscript Reverse Transcriptase kit (Qiagen). Real-time qRT-PCR was then performed by using 2× SYBR Green PCR Master Mix (Applied Biosystems) according to the manufacturer's instructions in the ABI PRISM 7500 system. The RT-PCR primers used in this study were: Lasp1, 5'-GTATCCCACGGAGAAGGTGA-3' (forward) and 5'-TGTCTGCCACTACGCTGAAA-3' (reverse); p53, 5'-CCAGGG-CAGCTACGGTTTC-3' (forward) and 5'-CTCCGTATGTG-CTGTGACTG-3' (reverse); p21, 5'-GACACCACTGGAGGG-TGACT-3' (forward) and 5'-GGATTAGGGCTTCCCTTG-G-3' (reverse); and housekeeping gene HPRT, 5'-GTAATG-CCAGTCAACAGGGGAC-3'(forward) and 5'-CCAGCAAG-CTTGCACCTTGACCA-3' (reverse).

Western Blot Analysis. The experimental cells were washed twice with PBS and then lysed in cell lysis buffer [50 mM Tris-HCl (pH 7.8), 150 mM NaCl, 1% Nonidet P-40] containing 1× complete mini protease inhibitor mixture (Roche Applied Science) and 1 mM PMSF (Sigma-Aldrich) on ice for 30 min. The lysates were centrifuged at 16,000 × g for 15 min at 4 °C, and the protein concentration was measured with a Bradford Protein Assay Kit (Bio-Rad). Proteins were separated by 10–12.5% SDS/PAGE and transferred to Hybond PVDF membranes (Amersham Pharmacia). Antibodies against Lasp1 (Chemicon International), p53 (DO-1) and p21 (Santa Cruz Biotechnology) were used as primary antibodies in this study for protein detection, followed by reacting to appropriate HRP-conjugated secondary antibodies (Dako). Equal loading of protein samples was verified with antibodies to β-actin (Chemicon International). After blotting with primary and secondary antibodies, the immunoreactive signals were visualized by reacting with enhanced chemiluminescence (ECL^{plus}) reagents (Amersham Pharmacia).

ChIP. ChIP assays were carried out by using HCT116 (*p53*^{+/+}) cells treated with 5-FU (375 μM) for 24 h. Briefly, cells were cross-linked with 1% formaldehyde (final concentration) (Sigma-Aldrich) for 10 min at room temperature. Formaldehyde was then inactivated by addition of 125 mM glycine. Then chromatin extracts containing DNA fragments of average size of 500 bp were immunoprecipitated by using anti-p53 DO1 mAb (Santa Cruz Biotechnology) and Dynabead Protein G (Invitrogen). After extensive wash of the immunoprecipitated complex, the DNA-protein complex was eluted in ChIP elution buffer. Finally, 2.5 M glycine was added to de-cross-link the protein from DNA. Then the phenol/chloroform-purified ChIP-DNA dissolved in TE buffer was ready as the template for ChIP-

qPCR. The analyses for the ChIP-qPCR were performed by using ABI PRISM 7900 Sequence Detection System and SYBR Green Master Mix (Applied Biosystems). Threshold cycles (C_t) were determined for both immunoprecipitated DNA and a known amount of DNA from the input sample for different primer pairs. Relative occupancy values (also known as fold enrichments) were calculated by determining the immunoprecipitation efficiency (ratios of the amount of immunoprecipitated DNA to that of the input sample) and normalized to the level observed at a control region, which was defined as 1.0. The control region is a 238-bp region at 2 kb upstream of Lasp1 transcription start site and is amplified by using the primers CHIP-Ctrl (-1,939 to -1,702 bp): CTCAGCTCATAG-GCAGGGCTTGGCTTGAT (forward) and CTGC-GATATTTAAACCCGGAATGTG (reverse).

The oligonucleotide sequences used in ChIP-qPCR were: CHIP-1 (-651 to -453 bp), AGAAAAAAGGGGTCAAGCT-GAACCGCAGACGG (forward) and GACCCCCTACCCTGC-CCCTCTTAGCTCTC (reverse); CHIP-2 (-326 to -191 bp): GGCGCCCCAGATGTGCAGCCTGCTCG (forward) and GGGCGGGTTCCTGGGGGGACGG (reverse); CHIP-3 (-92 to +96 bp), CTGTGTTATTAGGGGAAGGAGGGCG-GAGG (forward) and CCGGGCGCAGTTGGGTTATGG-TTCCGAG (reverse); CHIP-4 (-89 to +95 bp), TGTTTAT-TAGGGGAAGGAGGGCGGAGG (forward) and: CGGGC-GCAGTTGGGTTATGGTTCCGA (reverse); CHIP-5 (+251 to +449 bp), AGAATGGAGGGAGGGCGAGCGGG-CGGTGTC (forward) and CCTTCCCCAACACACCCCCGG-CGCCTGAC (reverse); CHIP-6 (+581 to +762 bp), GGCTG-GGGGGCCCTGCAAAACCGTC (forward) and CGACTGA-ATCCAAGGGGGTGCAGGTCGTTC (reverse).

ELISA. Briefly, streptavidin-precoated 96-well plate (Thermo) was rinsed with PBS twice and blocked in 3% BSA for 2 h at room temperature. Twenty-five nanograms of purified wild-type p53 protein (Aviva Systems Biology) was incubated in binding buffer (5 mM Tris, 0.5 mM EDTA, 50 mM KCl, pH 7.8) with monoclonal anti-p53 antibody DO-1 (1:1,000) for 10 min at room temperature. Different dilutions of annealed double-stranded biotin labeled DNA probes (2, 10, or 50 ng) were then added, mixed, and plated into streptavidin-coated plates for 20-min incubation at room temperature. Samples were drained and rinsed with PBST (0.1% Tween) once followed by PBS containing 0.1% BSA thrice. Goat-anti-mouse HRP-conjugated IgG (1:1,000 dilution) was added and incubated for 15 min at 4 °C. After extensive wash with PBST and PBS, 50 μL of TMB substrate (Sigma) was added and incubated for 5–10 min and the reaction was stopped by TMB stop reagent (Sigma). Measurement of color resulting from the enzymatic reaction was performed in a Tecan plate reader at 450/570-nm wavelength. The DNA probes used in this study were: Lasp1, biotin-aggCCAGt-tcgctCCAGccg (sense) and cggttggagcgaaCTGGcct (antisense); Lasp1-AT, biotin-aggCATGttcgctCATGccg (sense) and cggttggagcgaaCATGcct (antisense); p21, biotin-gaaCATGtc-ccaaCATGttg (sense) and caaCATGttgggaCATGttc (antisense); p21-CA, biotin-gaaCCAGtccaaCCAGttg (sense) and caaCTGGttgggaCTGGttc (antisense); and non-RE control, biotin-taaggctatgaagagatact (sense) and agtatcttcatagccta (antisense).

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Table S1. Validated p53REs

Gene	Function	p53RE			p53 function		
		Half-site 1 (RRRCWWGYYY)	Spacer [N _(0-13bp)]	Half-site 2 (RRRCWWGYYY)	Ref.	Published	Predicted
ACTA2	a	AACCAGCCT		GCATCTGCC	1	↑	↑
ADAR1/ADAR2/RED	k	GTGCAAGTT		CAACTTGCC	2	↑	↑
AEN	a	GGGCTTCCC		GGGCATGTGG	3	↑	↑
AIFM2/AMID/PRG3	a	AGGCATGAC	caccgtgcct	GGCCATGCC	1	↑	↑
APAF1	a	AGACATGCT	ggagacccttagga	CGACAAGCCC	1,2	↑	↑
ARHGEF7	h	AAACATGCA		GCACTTGCTT	2	↑	↑
ARID3A/E2FBP1	b	GGCACGCTG		GGACATGCC	1	↑	↑
ATF3	a,d,k	AGTCATGCC	ctggctgggaccatt	GGTCATGCC	1,2	↑	↑
BAI1	f	GTGGCTGCC		GGACATGTC	1	↑	↑
BAX	a	GGGCAGGCC		GGGCTTGTG	1	↑	↑
BBC3/PUMA	a	CTGCAAGTCC		TGACTTGCC	1,2	↑	↑
BCL6	n	AGACAGTCT	tgggggtgattc	GGGCTAGTCT	1	↑	↑
BID	a	GGGCATGATG		GTGCATGCC	1,2	↑	↑
BNIP3L	a	AAGCTAGTCT	cagtg	GCGCATGCC	1	↑	↑
C12orf5/TIGAR	a,m	AGACATGTC	ac	AGACTTGCT	1,2	↑	↑
CASP1	a	AGACATGCAT		ATGCATGCAC	1,2	↑	↑
CASP6	a	AGGCAAGGAG	tttg	AGACAAGTCT	1,2	↑	↑
CAV1	b,m	GCCCAAGCAC	cccagcgccc	AGAACAGTTC	1	↑	↑
CCNG1	b	GCACAAGCCC		AGGCTAGTCC	1	↑	↑
CCNK	b	AAACTAGCTT	gc	AGACATGCTG	1	↑	↑
CD82/KAI1	f	AGGCAAGCTG	gggca	GCTCAAGCCT	1	↑	↑
CDKN1A/p21	b,d	GAACATGTC		CAACATGTTG	1,2	↑	↑
CDKN1A/p21	b,d	GAAGAAGACT		GGGCATGTC	1,2	↑	↑
Chmp4C	m	AAACAAGCCC	agtagcagcagctgc	GAGTTGCC	1	↑	↑
COL18A1	f	TGACATGTGT		GAGCATGTAT	1	↑	↑
CX3CL1/fractalkine	j	GGGCATGTC	c	CAGTTG	1	↑	↑
DCC1	a	GAGCATGTC		ACACAAGCCA	2	↑	↑
DDB2	c	GAACAAGCCC	t	GGGCATGTT	1,2	↑	↑
DKK1	a	AGCCAAGCTT	ttaatg	AACCAAGTTC	1,2	↑	↑
DSC3	f	GAAGTTGCTC	ccggc	AGGCAAGCCT	2	↑	↑
DUSP1/MKP1	a,b	GGTCTGCC		AGGCAATGG	1	↑	↑
DUSP5	a,g	CAACAAGCCC	t	TGTCTAGTGC	1	↑	↑
EDN2	d,h	CTGCAAGCCC		GGGCTAGCCC	1,2	↑	↑
EEF1A1, E3	a,g	AAACATGATT	ac	AGGGACATCT	1	↑	↑
EEF1A1, E4	a,g	GGGCAGACCC	ga	GAGCATGCC	1	↑	↑
EEF1A1, E2	a,g	GGACACGTAG	attc	GGGCAAGTCC	1	↑	↑
EGFR	b,n	GAGCTAGACG	tcc	GGGCAGCCCC	1	↑	↑
EOMES/TBR2	e	GGGCCTGCT	c	CAACTGCC	2	↑	↑
EphA2/ECK	a	CACCATGTTG	gcc	AGGCATGTC	1	↑	↑
FANCC/FAC	a,c	GGACATGTT	aaatactga	GAGCTATTT	1	↑	↑
FAS/Apo-1/CD95	a	GGACAAGCCC		TGACAAGCCA	1,2	↑	↑
FDXR	a,m	GGGCAGGAGC		GGGCTGCC	1,2	↑	↑
FLT1	d	GGACATGTC	ccctg	GGACCTGAGC	2	↑	↑
FOS/c-FOS	a	ACGCTTCCA		TAGTAAGAAT	2	↑	↑
GADD45A	c	GAACATGTC		AAGCATGCTG	1,2	↑	↑
GDF15/MIC-1/PTGFB	h	AGCCATGCC		GGGCAAGAAC	1,2	↑	↑
GDF15/MIC-1/PTGFB	h	CATCTGCC		AGACTTGCT	1,2	↑	↑
GML	b	ATGCTGCC		AGGCATGTC	1	↑	↑
HD/Huntington	i	ATGCTTGTT	tacagaa	GAGCATGTTA	1	↑	↑
HD/Huntington	i	GGGCCTGCTT	ccagg	AAGCTTGCTT	1	↑	↑
HGF/SF	b,n	ACACATGAT		TTTCTGTTT	1	↑	↑
IBRDC2/P53RFP	b	AGACAGGTCC		TGACAAGCAG	1	↑	↑
IGFBP3	n	GGGCAAGACC		TGCCAAGCT	1,2	↑	↑
IGFBP3	n	AAACAAGCCA	c	CAACATGCTT	1,2	↑	↑
IRF5	j	AGGCATGCCA	ca	AGGCATGGTC	1	↑	↑
KRT8/CK8	g	CCGCCTGCC	cc	ACTCCTGCC	1	↑	↑
LIF	j	GGACATGTC		GGACAGCTCC	1	↑	↑
LRDD/PIDD	a	AGGCCTGCC	gcgtgctg	GGACATGTC	1,2	↑	↑
MDM2	n	AGTTAAGTCC		TGACTTGCT	1,2	↑	↑
MDM2	n	GGTCAAGTCC		AGACACGTT	1,2	↑	↑
MLH1	c	AAGCATGTAC	a	GCGCATGCC	1,2	↑	↑
MMP2	f	AGACAAGCCT		GAACATGTC	1,2	↑	↑

Gene	Function	p53RE			p53 function		
		Half-site 1 (RRRCWWGYYY)	Spacer [N _(0-13bp)]	Half-site 2 (RRRCWWGYYY)	Ref.	Published	Predicted
MSH2	c	AGGCTAGTTT	tttttttgttttc	AAGTTCCCTT	1	↑	↑
NDRG1	a	CCACATGCAC	acgcacgagcg	GCACATGAAC	1,2	↑	↑
NLRC4/IpaF	a	AGACATGTC		CTGGTAGTTT	1	↑	↑
P2RXL1/P2XM	i	GAACAAGGGC	at	GAGTTGTCT	1	↑	↑
P53AIP1	a	TCTCTTGCCC		GGGTTGCG	1,2	↑	↑
PCNA	a,c	GAACAAGTCC		GGGCATATGT	1	↑	↑
PDGFC/SCDGF	h	GGTCATGTT		AGACTTGCCC	2	↑	↑
PERP	a	AGGCAAGCTC		CAGCTTGTC	1,2	↑	↑
PLAGL1/ZAC	b,n	CAACTAGACT		AGACTAGCTT	1,2	↑	↑
PLK2/SNK	b	AAACATGCC		GGACTTGCCC	1,2	↑	↑
PMS2	c	ATACTTGATT	tg	TTTCTTGAA	1,2	↑	↑
PPM1J/MGC19531	h	GAACATGCC		GAGCAAGCCC	1,2	↑	↑
PRDM1/BLIMP1	j	GTGCAAGTCT		GGACATGTTT	1	↑	↑
PRKB1/AMPKbeta1	n	GTTCTTGCCG		CGGCTTGCTC	1,2	↑	↑
PTEN	a	GAGCAAGCCC	caggcagctacact	GGGCATGCTC	1	↑	↑
PYCARD/ASC	a	GTGCAAGCCC	ag	AGACAAGCAG	1	↑	↑
RABGGTA/PTAR3	?	CCTCTTGCGG	aacgtgca	AAGCCTGTC	1	↑	↑
RFWD2/COP1	n	AGACTTGCT	gt	GAACAGTCAC	1	↑	↑
RNPC1/RBM38	k	GGGCAAGTCC	aggcgccc	CCCCAAGCTC	4	↑	↑
RPS27L	e	GGGCATGTAG		TGACTTGCCC	1,2	↑	↑
RRM2B/P53r2	c	TGACATGCC		AGGCATGTC	1,2	↑	↑
S100A2	b	GGGCATGTGT		GGGCACGTT	1	↑	↑
SCARA3/CSR1	c,l	GGGCAAGCCC		AGACAAGTTG	1,2	↑	↑
SCGB1D2/LIPB	h	GGTCTTGTTT		AGACTTGCTC	2	↑	↑
SCN3B	a	TGACTTGCTC		TGCCCTGCT	1	↑	↑
SCN3B	a	TGGCAAGGCT		GAGCTAGTC	1	↑	↑
SEMA3B	e	TTGCATGCC	ag	AGACATGTC	2	↑	↑
SERPINB5/maspin	f	GAACATGTTG	g	AGGCCTTTG	1,2	↑	↑
SERPINE1	f	ACACATGCCT		CAGCAAGTCC	1,2	↑	↑
SERTAD1	d	GGGCATGGC		CCTCAAGCCC	2	↑	↑
SESN1/PA26	a,d	GGACAAGTCT		CCACAAGTCA	1,2	↑	↑
SFN/14-3-3 sigma	b	TAGCATTAGC	cc	AGACATGTC	1,2	↑	↑
SOD2/MnSOD	l	GTGCTTGTC	taaa	GGGCATGTC	2	↑	↑
STAG1	a	GGGCTTGCT	g	GCACATGTC	5	↑	↑
STEAP3/TSAP6	f,m	AGACAAGCAT	ag	GGACATGCTC	1	↑	↑
TAP1	n	GGGCTTGCC	ctggcg	GGACTTGCT	1	↑	↑
TGFA	a,n	GGGCAGGCC		TGCCCTAGTC	1,2	↑	↑
TNFRSF10A/DR4	a	GGGCATGTC		GGGCAGGAGG	1	↑	↑
TNFRSF10B/DR5/KILLER	a	GGGCATGTC		GGGCAAGACG	1,2	↑	↑
TNFRSF10C/DcR1	a	GGGCATGTC		GGGCAGGACG	1,2	↑	↑
TNFRSF10D/DcR2	a	GGGCATGTC		GGGCAGGACG	1	↑	↑
TP53/p53	a,b,c,d	TTACTTGCC		TTACTTGTCA	1	↑	↑
TP53I3/PIG3	a	CAGCTTGCC		ACCCATGCTC	2	↑	↑
TP53INP1	a	GAACTTGGGG		GAACATGTTT	1	↑	↑
TP63/TP73L	n	TAACCTGTTA	ttg	AAACATGCTC	1	↑	↑
TP73/p73	n	CAACTTGAG	agtaagctgga	GAGCTGAAT	1	↑	↑
TP73/p73	n	CTACTTGCG	tccgggaa	GAACTTGCAG	1	↑	↑
TP73:Delta	n	GGGCAAGCTG		AGGCCTGCC	1,2	↑	↑
TRAF4/CART1/MLN62	a	GGGCAAGCCA		GGGCCTGCC	2	↑	↑
TRIAP1/p53CSV	a	CTTCATGTC		GTGCATGCC	1	↑	↑
TRIM22/Staf50	c	TGACATGTC		AGGCATGTC	1	↑	↑
TSC2/LAM	n	GGGCATGGTG		GCACATGCC	1	↑	↑
TSC2/LAM	n	TAACAAGCTC	g	GGGCTAGCCC	1	↑	↑
UBTD1	h	GAGCAAGCCC		AGACTTGCA	2	↑	↑
VCAN/CSPG2	b	AGACTTGCA	c	AGACAAGTCC	1	↑	↑
VDR	a,b	TAACCTAGTT		GAACAAGTTG	1	↑	↑
VDR	a,b	AGGTTAGATG	tac	TAACCTAGTT	1	↑	↑
WIG1/ZMAT3	a	AAACAAGTCC		AGACATGCC	2	↑	↑
XRCC5/KARP-1/Ku86	c	GAACTAGTTT	t	AAACATGTC	2	↑	↑
ABCBL1/MDR1	m	GGGCAGGAAAC	agcggcgccccgt	GGGCTGAGCA	1	↓	↓
AFP	e	AAACATGTC	gga	CCTCTAGACA	6	↓	↓
ANLN	g	GAACCTGGCTT	ttctga	GGGCCAAGCC	1	↓	↓
AR	h	CAGCAACTAT		CTGCTGGCTT	7	↓	↓

Gene	Function	p53RE			p53 function		
		Half-site 1 (RRRCWWGYYY)	Spacer [N _(0-13bp)]	Half-site 2 (RRRCWWGYYY)	Ref.	Published	Predicted
FOS/c-FOS	a	GAGCGCACGC		ACGCTTGCCA	2	↓	↓
FOS/c-FOS	a	GGACTTGCTC	t	GAGCGCACGC	2	↓	↓
GDF15/MIC-1/PTGFB	h	CTCCCAGGCT		GGAATGGTGT	8	↓	↓
LASP1/MLN50	g	AGGCCAGTTC	ccca	GCTCCAGCCG	9	↓	↓
LGALS3/galectin-3	a	GGGCTTGCAA	gctgg	AGCCTTGTTT	1	↓	↓
MAD1L1/MAD1	b	ATTCAAGCTG		ATACTGAGTA	1	↓	↓
Nanog	k	CAGCAAGGTC	tgactc	TTTCATGTCT	10	↓	↓
ODC1	b	GGACCAGTTC	caggc	GGGCGAGACC	1	↓	↓
ODC1	b	GGGCTCGCCT	tggtacagac	GAGCGGGCCC	1	↓	↓
POLD1	k	GAACAAGCGG	ggcgt	GGCCTTGCCC	11	↓	↓
RAD51/BRCC5	c	AAACTCGCGC	ag	GATCAAGCTC	12	↓	↓
RAD51/BRCC5	c	GATCAAGCTC	tcgagctcc	CGTCTGGGT	12	↓	↓
RB1	b	GGGCGTGCC	cgac	GTGCGCGCGC	1	↓	↓
SCD	f	GGGCCGGTCC	t	GGGCTAGGCT	1	↓	↓
TauT	i	AACCAAGACA	cagaaggctggg	GAACTTGCCT	13	↓	↓
TRPM2	b, i	GGCCTTGCTT	tgctc	AGGCCTGCTT	1	↓	↓
UBD/FAT10	a	AGGCATGCTC		AGTGGCGTGG	1	↓	↓

Function: a, apoptosis; b, cell cycle regulation; c, DNA repair; d, cell growth and senescence; e, cell fate and development; f, ECM (extracellular matrix) and adhesion; g, cytoskeleton; h, cell signaling; i, central nervous system; j, immune system; k, transcription/translation regulation; l, ROS regulation; m, cellular metabolism; n, regulator of p53. ?, function unknown. ↑, activated by p53; ↓, repressed by p53.

Table S2. Reassignment of 20 discrepant p53 REs

Gene	Function	p53RE			p53 function			
		Half-site (RRRCWWGYYY)	Spacer [N _(0-13bp)]	Half-site (RRRCWWGYYY)	Ref.	Published	Predicted	Test*
AIFM2/AMID	a	GGTCTCGCTA	tgttccc	AGGCTGGTCT	1	↑	↓	↓ (-57.5%)
BCL2L14/BCL-G	a	AGCCAAGGCT		GGTCTTGAAC	14	↑	↓	↓ (-63.3%)
BDKRB2/BK2	j	GGAAGTGCCC		AGGAGGCTGA	1	↑	↓	↓ (-60.1%)
BIRC5/survivin	a	GGGCGTGC	tcc	CGACATGCC	1	↓	↑	↑ (+28.5%)
BTG2/TIS21/PC3	b	AGTCGGGCA	g	AGCCCGAGCA	1	↑	↓	↓ (-21.6%)
C13orf15/RGC32	b	AGGCAGATT	aag	CAGCTTGTCC	1	↑	↓	↓ (-57.9%)
CTSD/IRDD	a	AACCTTGGTT	tg	CAAGAGGCTT	15	↑	↓	↓ (-62.3%)
CTSD/IRDD	a	AAGCTGGCC		GGGCTGACCC	15	↑	↓	↓ (-63.3%)
DDIT4/REDD1	c, l	AAACAAAGTCT		TTCCTTGTAC	1	↑	↓	↓ (-39.3%)
DDR1	d, n	GAGCTGGTCC		AGGCTTATCT	1	↑	↓	↓ (-46.2%)
EOMES/TBR2	e	GGGCCCTGTCT	c	CAAATCGCCC	2	NA	↓	↓ (-31.0%)
FLT1	d	GGACACGCTC	ccctg	GGACCTGAGC	2	NA	↓	↓ (-62.3%)
HD/Huntington	i	CGCCATGTTG	gcc	AGGCTGGTCT	1	↑	↓	↓ (-55.3%)
IER3/IEX-1	a	CCACATGCCT		CGACATGTGC	16	↓	↑	↑ (+144.2%)
MSH2	c	GACCTAGGCG	c	AGGCATGCGC	1	↑	↓	↓ (-62.1%)
Notch1	e	GGCCACGCCA		AGCCATGGTC	17	↑	↓	↓ (-65.9%)
Notch1	e	AATCACGGCC		AGGGATGTCT	17	↑	↓	↓ (-56.8%)
PLK2/SNK	b	GGTCATGATT	cct	TAACTTGCCT	18	↑	↓	↓ (-61.3%)
PML	a, d, k	GCGCTGGCCT	ggagccag	GGGCATGTCC	1	↑	↓	↓ (-24.4%)
TSC2	n	AGGCTAGTCT	gaaa	CTCCCTGGGC	1	↑	↓	↓ (-57.6%)

Function: a, apoptosis; b, cell cycle regulation; c, DNA repair; d, cell growth and senescence; e, cell fate and development; f, ECM (extracellular matrix) and adhesion; g, cytoskeleton; h, cell signaling; i, central nervous system; j, immune system; k, transcription/translation regulation; l, ROS regulation; m, cellular metabolism; n, regulator of p53. ↑ shows activation by p53. ↓ shows repression by p53. NA: information not available.

*Luciferase assay results are shown as % reduction or gain relative to pcDNA3.1 control.